

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 15, 2002, 17:31:55 ; Search time 1398.01 Seconds
(without alignments)
8543.543 Million cell updates/sec

Title: US-09-762-633-3
724

Perfect score: 1 gaagtcgtacaaagtgagcc.....gatgttaccgggaagttaca 724

Sequence: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Scoring table: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_dat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_om:*
20: em_or:*
21: em_ov:*
22: em_pat:*
23: em_ph:*
24: em_pl:*
25: em_ro:*
26: em_sts:*
27: em_sy:*
28: em_un:*
29: em_vl:*
30: em_htgo_hum:*
31: em_htgo_inv:*
32: em_htgo_rod:*
33: em_htg_hum:*
34: em_htg_inv:*
35: em_htg_rod:*
36: em_htg_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	724	100.0	724	1	AB022061 Pectinatu
2	318.8	44.0	624	1	AB022063 Pectinatu
3	238.4	32.9	399	1	AB022062 Pectinatu
4	169	23.3	579	1	AB022094 Selenomon
5	163.8	22.6	442	1	AB022064 Pectinatu
6	119.2	16.5	467	1	AB040730 Clostridi
7	117.6	16.2	467	1	AB040727 Clostridi
8	117.4	16.2	417	1	AB040726 Clostridi
9	117.4	16.2	417	1	AB040737 Clostridi
10	114.2	15.8	413	1	AB040729 Clostridi
11	113.8	15.7	505	1	AB040724 Clostridi
12	111.8	15.4	5986	1	CJ1168X2
13	111.8	15.4	308601	1	CJ11168X1
14	111.8	15.4	314150	1	CJ11168X1
15	111.8	15.4	317511	1	CJ11168X3
16	110.4	15.2	460	1	AB040723 Clostridi
17	110.4	15.2	968	1	AF146727 Campyloba
18	108.8	15.0	441	1	AB040542 Clostridi
19	108.8	15.0	479	1	AB040714 Clostridi
20	108.8	15.0	551	1	AB040717 Clostridi
21	106	14.6	556	1	AB040720 Clostridi
22	102.8	14.2	750	1	AB074835 Campyloba
23	102.8	14.2	751	1	AB074830 Campyloba
24	102.8	14.2	914	1	AF074840 Campyloba
25	102.8	14.2	946	1	AF074839 Campyloba
26	102.6	14.2	2423	1	AB066098 Campyloba
27	102	14.1	751	1	AF074832 Campyloba
28	101.8	14.1	752	1	AF074834 Campyloba
29	101.6	14.0	753	1	AF074828 Campyloba
30	101.4	14.0	751	1	AF074833 Campyloba
31	100.4	13.9	750	1	AF074831 Campyloba
32	100.4	13.9	778	1	AF074836 Campyloba
33	100.4	13.9	823	1	AF074837 Campyloba
34	100	13.8	812	1	AF074838 Campyloba
35	99.6	13.8	632	1	AF074829 Campyloba
36	97	13.4	632	1	AF074841 Campyloba
37	94.4	13.0	511	1	AF203394 Xanthomon
38	94	13.0	493	1	AB004288 Xanthomon
39	94	13.0	493	1	AF035441 Xanthomon
40	94	13.0	494	1	AB004284 Xanthomon
41	94	13.0	494	1	AB004289 Xanthomon
42	94	13.0	502	1	AF279422 Xanthomon
43	94	13.0	502	1	AF279423 Xanthomon
44	94	13.0	502	1	AF279424 Xanthomon
45	94	13.0	502	1	AF279425 Xanthomon

ALIGNMENTS

RESULT 1
AB022061 724 bp DNA BCT 30-MAR-2000
LOCUS
DEFINITION Pectinatus cerevisiiphilus DNA, 16S/23S rRNA intergenic spacer
REGION
ACCESSION AB022061
VERSION AB022061.1 GI:7288087
SOURCE
KEYWORDS
ORGANISM Pectinatus cerevisiiphilus (strain:DSM20467) DNA.
Pectinatus cerevisiiphilus
Bacteria; Firmicutes; Bacillus/Clostridium group; Sporomusa
subbranch; Selenomonadaceae; Pectinatus.
REFERENCE
1 (sites)
Motoyama, Y. and Ogata, T.
16S-23S rDNA spacer of Pectinatus, Selenomonas and Zymophilus
reveal new phylogenetic relationships between these genera
Int. J. Syst. Evol. Microbiol. 50 Pt 2, 883-886 (2000)
JOURNAL MEDLINE
20222199
2 (bases 1 to 724)
Ogata, T. and Motoyama, Y.

TITLE Direct Submission
JOURNAL Submitted (07-JAN-1999) to the DDBJ/EMBL/GenBank databases. Tomoo

Ogata, Asahi Breweries, Ltd., Brewing Research and Development
Laboratory; 1-1-21, Midori, Moriya, Ibaraki 302-0106, Japan
(E-mail:tomoo.ogata@asahibeer.co.jp, Tel:81-297-46-1513,
Fax:81-297-46-1514)

FEATURES
Location/Qualifiers

1..724

/organism="Pectinatus cerevisiiphilus"

/strain="DSM20467"

/db_xref="taxon:86956"

misc_feature

BASE COUNT 257 a 121 c 187 g 159 t

ORIGIN

Query Match 100.0%; Score 724; DB 1; Length 724;
Best Local Similarity 100.0%; Pred. No. 9,4e-105;
Matches 724; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
1 ggaatcglaacaaggtagccgtatcgaagaagtcgagcgtgatacctcttctaagat 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
J GAAGTCGTACACAGTACCGCTATCGAAGGTCGGCTGGATCACCTCTTCTAAGCAT 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
61 ttgacaaaatctctcgatcatccggaatatagtatgttctgttcttgaggtcttc 120
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
61 ttgacaaaatctctcgatcatccggaatatagtatgttctgttcttgaggtcttc 120
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
121 cctcaaatatatagtatactctgttaagatgtttatgatatgtttaaaagctgcg 180
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
121 CTCATAAATATATAGTACATCTGTGTAGAGTGTATGATGATTTTAAAGCTGGCG 180
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
181 aaatatgtgtgcaaaaaaagcattgacgtagagaagactggttaaaaaaagatga 240
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
181 AAATATTGCTGCAAAAAAAATGCCATGCGACTAGACAAAGACTGTAAAAAAGATGA 240
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
241 taatggggggttaactcagatggtgagacacctgacctgcaaggagggtcaagatc 300
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
241 TAAATGGGGGCTACCTCAGATGGAGACACTCTCTTGCACAGCGGGCTCAGGATTC 300
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
301 aactctctctgtctccaccagaagaagagcctatactagctcagcttggttagagcg 360
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
301 AACCTCCTCTGTCCACACAGACGAAGGGCTTATAGCTCAGCTGTAGAGCGCAGC 360
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
361 cctgataagcttgaggtcagtaattcaagcttaagccaccacataltgacattga 420
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
361 CCTGATTAAGCCTGAGGTCAGTAGTTCAAAGCTCTACTTAGCCCAATATTGCCAAT 420
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
421 aaactacacagaagaagaacaaacatactacacaaacttgaagaagaatc 480
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
421 AAATCTACACGAAGAAGCAAAAGACAAATTAATCACCAATGCCAACTTGTAAAGAA 480
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
481 gaggagaagatgagcgaatgatttgacaaagcacaaattagaaagaagaacacgt 540
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
481 GAGGAGAGAAATGGCGCGAATAGTTGGACCAACCAAAATATTAGCAAAAGAAACG 540
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
541 aagaaacaacataataaacttaagcgaagaaggtatattcttgagaagaactcaga 600
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
541 AAGAAACAACATATAACTTTAAGCCAAAAGGTGATATCTTGAGGAACCTTCAGAT 600
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
601 ataacttaccagaagcgttcagatgcaaggaagcgaagcttgaagaagaagcgtat 660
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
601 ATTAACCTTACCAAGCGTTCAGATCCGAGGAAGGGCAAGCTGACAGAAAGAGCT 660
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
661 taatatagctgttgaagaagaagcactgaacaagcagatgagttatgggaagt 720
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
661 TAAATATACCTGTATGAACGACGAAGCACTGACAAAGCAGATGATGCTTATGGAA 720
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
721 taca 724
| | | | |
721 TACA 724
```

RESULT 2

AB022063

LOCUS

DEFINITION

AB022063

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

REFERENCE

AUTHORS

TITLE

```

SOURCE
1..467
/organism="Clostridium novyi"
/db_xref="taxon:1542"
rRNA
complement(<1..30)
/product="16S ribosomal RNA"
tRNA
complement(156..231)
/product="tRNA-Ala"
complement(239..315)
/product="tRNA-Ile"
complement(402..>467)
/product="23S ribosomal RNA"
BASE COUNT      139 a      84 c      112 g      132 t
ORIGIN

Query Match
Best Local Similarity 82.6%  Pred. No. 1.5e-09;
Matches 147; Conservative 0; Mismatches 29; Indels 2; Gaps 1;

QY 234 atgaactaagggcgtagctcagatgagagagcacccttccttgcagaagggtca 293
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 145 AATTTACTAGTGGGGCTATAGCTAGTGGAGACACCTGCTTGCACGCGGGGGTCA 204
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 294 ggaagttcaactctcctcgtctccaccagaagaagggcctatagctcagctgttaga 353
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 205 AGACTTCGAATCTCTTATCTCCACACATA--CAATGCGCTCTATAGCTCAGCTGCTTACA 262
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 354 ggcgcagcctataagcgtagtgcagtagtcaagcttaagcttaagccccaattat 411
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 263 GCGCACGCTGATTAAGCGGTGAGTGGATGTTGAGTCCATTGACCCACCATTTGTT 320
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 8
AB040726 417 bp DNA BCT 04-JAN-2001
LOCUS      Clostridium novyi genes for 16S rRNA, tRNA-Ala, tRNA-Ile, 23S rRNA,
DEFINITION partial and complete sequence.
ACCESSION AB040726
VERSION    AB040726.1 GI:12039003
KEYWORDS   16S ribosomal RNA; 16S rRNA; 23S ribosomal RNA; 23S rRNA.
SOURCE      Clostridium novyi (strain:ATCC25758) DNA.
ORGANISM    Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
            Clostridium.
REFERENCE   1 (sites)
AUTHORS     Sasaki,Y., Yamamoto,K., Kojima,A., Norimatsu,M. and Tamura,Y.
TITLE       Rapid identification and differentiation of pathogenic clostridia
            in gas gangrene by polymerase chain reaction based on the 16S-23S r
            DNA spacer region
JOURNAL     Res. Vet. Sci. 69 (3), 289-294 (2000)
PUBMED      11124102
2 (bases 1 to 417)
DIRECT SUBMISSION
SUBMITTED (26-MAR-2000) Yoshimasa Sasaki, National Veterinary Assay
Laboratory, Assay Division 1; 1-15-1 Tokura, Kokubunji, Tokyo
185-8511, Japan (E-mail:sasakiy@nval.go.jp,
Tel:+81-42-321-1841(ex.230), Fax:+81-42-321-1769)
FEATURES
source
1..417
/organism="Clostridium novyi"
/db_xref="taxon:1542"
complement(<1..30)
/product="16S ribosomal RNA"
tRNA
complement(106..181)
/product="tRNA-Ala"
complement(185..261)
/product="tRNA-Ile"
complement(352..>417)
/product="23S ribosomal RNA"
BASE COUNT      125 a      83 c      103 g      106 t

```

```

ORIGIN

Query Match
Best Local Similarity 16.2%  Score 117.4; DB 1; Length 417;
Matches 167; Conservative 0; Mismatches 36; Indels 8; Gaps 2;

QY 243 atggggcgtagctcagatggaagagcactgccttcgaagggggtcagaattcaa 302
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 104 ATGGGGGATATAGCTCATTTGGAGAGACCTGCTTCACGACAGGGGCTGAAGATTGCA 163
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 303 ctctccctcgtctccaccagaagaaggcctatagctcagctggttagagcgacgac 362
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 164 ATCTCTTATCTCCACCA-----TAAGGCTTATAGCTCAGCTGTTAGAGCGACGCC 217
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 363 tgataagcgtagtgcagtagtgcagcttaagcttaagccccaattatgacattgaa 422
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 218 TGATTAAGCGTAGAGTGCATGCTGAGTCCATTGACCCACCA--ATTGTTCTTTGAAA 275
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 423 actacacagaagaagcaagaacattalc 453
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 276 ATTGCACAGTGAATAAGAAACGAAAAAAC 306
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 9
AB040737 514 bp DNA BCT 04-JAN-2001
LOCUS      Clostridium perfringens genes for 16S rRNA, tRNA-Ala, tRNA-Ile, 23S
DEFINITION rRNA, partial and complete sequence.
ACCESSION AB040737
VERSION    AB040737.1 GI:12039014
KEYWORDS   16S ribosomal RNA; 16S rRNA; 23S ribosomal RNA; 23S rRNA.
SOURCE      Clostridium perfringens (strain:JCM1290) DNA.
ORGANISM    Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
            Clostridium.
REFERENCE   1 (sites)
AUTHORS     Sasaki,Y., Yamamoto,K., Kojima,A., Norimatsu,M. and Tamura,Y.
TITLE       Rapid identification and differentiation of pathogenic clostridia
            in gas gangrene by polymerase chain reaction based on the 16S-23S r
            DNA spacer region
JOURNAL     Res. Vet. Sci. 69 (3), 289-294 (2000)
PUBMED      11124102
2 (bases 1 to 514)
DIRECT SUBMISSION
SUBMITTED (26-MAR-2000) Yoshimasa Sasaki, National Veterinary Assay
Laboratory, Assay Division 1; 1-15-1 Tokura, Kokubunji, Tokyo
185-8511, Japan (E-mail:sasakiy@nval.go.jp,
Tel:+81-42-321-1841(ex.230), Fax:+81-42-321-1769)
FEATURES
source
1..514
/organism="Clostridium perfringens"
/db_xref="taxon:1502"
complement(<1..30)
/product="16S ribosomal RNA"
tRNA
complement(191..266)
/product="tRNA-Ala"
complement(272..348)
/product="tRNA-Ile"
complement(449..>514)
/product="23S ribosomal RNA"
BASE COUNT      170 a      95 c      115 g      134 t

```

```

Query Match
Best Local Similarity 77.9%  Score 117.4; DB 1; Length 514;
Matches 169; Conservative 0; Mismatches 41; Indels 7; Gaps 2;

QY 243 atggggcgtagctcagatggaagagcactgccttcgaagggggtcagaattcaa 302
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

```
Db 189 ATGGGCGTATAGCTCAGTTGGAGAGCACCTGCTTGCACGCGAGGGGTCACAGACTTGA 248
QY 303 cttctcgtcgtccaccagaagaaggcctatagctcaagtcgttagagcgagcc 362
Db 249 ATCTCTTACCTCCACCAATATG----TGGGTCTATAGCTCAGAGTGGTTAGACCGCAGCC 304
QY 363 lntaaagctgaagtagtcaagtagtcaagtagtcaagtagtcaagtagtcaagtagtcaag 422
Db 305 TCATAGCGCTGAGCTGCATGCTTCGAGTCGCTTATAGACCCAGC---ATTGTTCTTTGAAA 361
QY 423 actcaccagaagaagaagaacatataccaat 459
Db 362 ATTGCACATTAATTATATAGAACACAGCCAAAT 398

RESULT 10
AB040729 413 bp DNA BCT 04-JAN-2001
LOCUS Clostridium haemolyticum genes for 16S rRNA, tRNA-Ala, tRNA-Ile,
DEFINITION 23S rRNA, partial and complete sequence.
ACCESSION AB040729
VERSION AB040729.1 GI:12039006
KEYWORDS 16S ribosomal RNA; 16S rRNA; 23S ribosomal RNA; 23S rRNA.
SOURCE Clostridium haemolyticum (strain:ATCC9650) DNA.
ORGANISM Clostridium haemolyticum
Bacteria: Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
Clostridium.
REFERENCE 1 (sites)
AUTHORS Sasaki,Y., Yamamoto,K., Kojima,A., Norimatsu,M. and Tamura,Y.
TITLE Rapid identification and differentiation of pathogenic clostridia
in gas gangrene by polymerase chain reaction based on the 16S-23S r
DNA spacer region
Res. Vet. Sci. 69 (3), 289-294 (2000)
11124102
2 (bases 1 to 413)
Sasaki,Y. and Tamura,Y.
Direct Submission
Submitted (26-MAR-2000) Yoshimasa Sasaki, National Veterinary Assay
Laboratory, Assay Division 1; 1-15-1 Tokura, Kokubunji, Tokyo
185-8511, Japan (E-mail:sasakiy@nval.go.jp,
Tel:+81-42-321-1841(ex.230), Fax:+81-42-321-1769)
FEATURES
source
1..413
Location/Qualifiers
/organism="Clostridium haemolyticum"
/strain="ATCC9650"
/db_xref="taxon:84025"
complement(<1..30)
/product="16S ribosomal RNA"
complement(106..181)
/product="tRNA-Ala"
complement(185..261)
/product="tRNA-Ile"
complement(348..>413)
/product="23S ribosomal RNA"
BASE COUNT 121 a 82 c 103 g 107 t
ORIGIN

Query Match 15.8%; Score 114.2; DB 1; Length 413;
Best Local Similarity 79.5%; Pred. No. 5.3e-09;
Matches 163; Conservative 0; Mismatches 33; Indels 9; Gaps 2;
```

```
QY 423 actacagaagaagaagaaga 447
Db 275 ATTGCACAGTATTAAGAAACGAAA 299

RESULT 11
AB040724 505 bp DNA BCT 04-JAN-2001
LOCUS Clostridium novyi genes for 16S rRNA, tRNA-Ala, tRNA-Ile, 23S rRNA,
DEFINITION partial and complete sequence.
ACCESSION AB040724
VERSION AB040724.1 GI:12039001
KEYWORDS 16S ribosomal RNA; 16S rRNA; 23S ribosomal RNA; 23S rRNA.
SOURCE Clostridium novyi (strain:JCM1406) DNA.
ORGANISM Clostridium novyi
Bacteria: Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
Clostridium.
REFERENCE 1 (sites)
AUTHORS Sasaki,Y., Yamamoto,K., Kojima,A., Norimatsu,M. and Tamura,Y.
TITLE Rapid identification and differentiation of pathogenic clostridia
in gas gangrene by polymerase chain reaction based on the 16S-23S r
DNA spacer region
Res. Vet. Sci. 69 (3), 289-294 (2000)
11124102
2 (bases 1 to 505)
Sasaki,Y. and Tamura,Y.
Direct Submission
Submitted (26-MAR-2000) Yoshimasa Sasaki, National Veterinary Assay
Laboratory, Assay Division 1; 1-15-1 Tokura, Kokubunji, Tokyo
185-8511, Japan (E-mail:sasakiy@nval.go.jp,
Tel:+81-42-321-1841(ex.230), Fax:+81-42-321-1769)
FEATURES
source
1..505
Location/Qualifiers
/organism="Clostridium novyi"
/strain="JCM1406"
/db_xref="taxon:1542"
complement(<1..30)
/product="16S ribosomal RNA"
complement(157..232)
/product="tRNA-Ala"
complement(236..312)
/product="tRNA-Ile"
complement(440..>505)
/product="23S ribosomal RNA"
BASE COUNT 157 a 92 c 118 g 138 t
ORIGIN

Query Match 15.7%; Score 113.8; DB 1; Length 505;
Best Local Similarity 74.9%; Pred. No. 5.8e-09;
Matches 158; Conservative 0; Mismatches 47; Indels 6; Gaps 1;
```

```

DEFINITION      C.jejuni TGH9011(ATCC43431) gene for ribosomal RNA operon.
ACCESSION       229326
VERSION         1
KEYWORDS        16S ribosomal RNA; 23S ribosomal RNA; 5S ribosomal RNA; transfer
SOURCE          RNA-Ala: transfer RNA-1le.
ORGANISM        Campylobacter jejuni.
Bacteria: Proteobacteria; epsilon subdivision; Campylobacter group;
Campylobacter.
REFERENCE       1 (bases 1 to 5996)
AUTHORS        Kim,N.W., Gutell,R.K. and Chan,V.L.
TITLE          Complete sequences and organization of the rRNA operon from
               Campylobacter jejuni TGH9011 (ATCC43431)
JOURNAL        Gene 164 (1), 101-106 (1995)
MEDLINE        96060846
REFERENCE       2 (bases 1 to 5996)
AUTHORS        Chan,V.V.
TITLE          Direct Submission
JOURNAL        Submitted (05-JAN-1994) Chan V. V., University of Toronto,
               Microbiology, 150 College Street, Toronto, Ontario, Canada, M5S 1A8
FEATURES        Location/Qualifiers
SOURCE          1..5996
               /organism="Campylobacter jejuni"
               /strain="TGH9011(ATCC43431)"
               /db_xref="taxon:197"
               /chromosome="genomic segment"
               /germline
               77..82
               /citation=[1]
               /label=-35seq165
               -10_signal
               98..103
               /citation=[1]
               /label=-10seq165
               264..1776
               /gene="rrs"
               /citation=[1]
               /product="16S ribosomal RNA"
               /evidence=experimental
               264..1776
               /gene="rrs"
               1881..1956
               /standard_name="alanine tRNA"
               /note="codon recognized: GCA"
               /citation=[1]
               /product="tRNA-Ala"
               /anticodon="(pos:1914..1916,aa:Ala)"
               /evidence=experimental
               1965..2041
               /standard_name="isoleucine tRNA"
               /note="codon recognized: AUC"
               /citation=[1]
               /product="tRNA-1le"
               /anticodon="(pos:1999..2001,aa:1le)"
               /evidence=experimental
               2582..5471
               /gene="rrl"
               /note="large subunit rRNA"
               /citation=[1]
               /product="23S ribosomal RNA"
               /evidence=experimental
               2582..5471
               /gene="rrl"
               5717..5836
               /citation=[1]
               /product="5S ribosomal RNA"
               /evidence=experimental
BASE COUNT     1833 a 1082 c 1476 g 1605 t
ORIGIN
Query Match    15.4%; Score 111.8; DB 1; Length 5996;
Best Local Similarity 74.4%; Pred. No. 5.9e-09;
Matches 154; Conservative 0; Mismatches 52; Indels 1; Gaps 1;

```

```

QY 217 aaagctgtaaaaaaagaatgaactaataggggcgtagctcaatgagagacctgcc 276
      |||||  |||  |  |||||  |||||  |||||  |||||  |||||  |||||
DB 1853 AAGATGATCATATAAGCTAATGTTATGGGGAATTAGCTACAGCTGGAGACGGCTGCT 1912
QY 277 ttccaagcagggggtcaggaggttcaactctccgtctccaccagaagaaggagccta 336
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 1913 TTGCACCCAGGAGGTGCGCGTTGATCCCGTATTCTCCACCA-TTTATTAAAGGCCCTA 1971
QY 337 tagctcagctggttaagcgcacgcctgataagcgtgagtcagttcaagttactt 396
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 1972 TAGCTCAGCTGTTAGAGTGCACCCCTGATTAAGGAGTACAGAGTTCAAGTTGTT 2031
QY 397 agggccaccacaatatgcacattgaaaa 423
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 2032 AGGCCACCACTAATAAAGATTTCGAATA 2058

RESULT 13
LOCUS      Cj11168X2 308601 bp DNA 08-JUL-2000
DEFINITION Campylobacter jejuni NCTC11168 complete genome; segment 2/6.
ACCESSION  AL139075 AL111168
VERSION     AL139075.2 GI:6967817
KEYWORDS
SOURCE      Campylobacter jejuni.
            Bacteria: Proteobacteria; epsilon subdivision; Campylobacter group;
            Campylobacter.
REFERENCE   1 (bases 1 to 308601)
AUTHORS     Parkhill,D., Wren,B.W., Mungall,K., Kellley,J.M., Churcher,C.,
            Basham,D., Chillingworth,T., Davies,R.M., Feltham,T., Holtroft,S.,
            Jagers,K., Karlyshev,A., Moule,S., Pallen,M.J., Penn,C.W.,
            Quail,M., Rajandream,M.A., Rutherford,K.M., VanVleet,A.,
            Whitehead,S. and Barrett,B.G.
            The genome sequence of the food-borne pathogen Campylobacter jejuni
            reveals hypervariable sequences
            Nature 403 (6770), 665-668 (2000)
            20150912
            2 (bases 1 to 308601)
            Parkhill,D.
            Direct Submission
            Submitted (09-FEB-2000) Submitted on behalf of the Campylobacter
            sequencing team, Sanger Centre, Wellcome Trust Genome Campus,
            Hinxton, Cambridge CB10 1SA E-mail: parkhill@sanger.ac.uk
COMMENT     Details of C. jejuni sequencing at the Sanger Centre are available
            on the World Wide Web.
            (URL, http://www.sanger.ac.uk/Projects/C.jejuni/).
            Location/Qualifiers
FEATURES     source
            1..308601
               /organism="Campylobacter jejuni"
               /strain="NCTC 11168"
               /db_xref="taxon:197"
               complement(101..886)
               /gene="Cj0343c"
               complement(101..886)
               /gene="Cj0343c"
               /note="Cj0343c, probable integral membrane protein, len:
               261 aa; similar to many hypothetical membrane proteins
               e.g. Y441_MENJA MJ0441 (267 aa), fasta scores: opt: 152
               z-score: 301.8 E(1): 1.5e-09, 30.7% identity in 257 aa
               overlap: 45.1% identity to HP0226"
               /codon_start=1
               /transl_table=11
               /product="putative integral membrane protein"
               /protein_id="CAB74180.1"
               /db_xref="GI:6967818"
               /translation="MEITDLPYLIIIGTIGTASGFGTGGMTTPSPFALGASAHHA
               IGISVLMFAVPGSYINYYKKNLKDGIMICGGGILGASFGSKMLKLSVALTS
               VLAIVSCIFPIYARGIKENIVONORSVWNVILIFAGATGIFALSLDIGGLLA
               PLIAIFLGIDSKKVVSLSPFYFASVSGIISFSNSGIDSEVIHKQILWGIASMGV

```

```

gene
    FIGIKIEKMHISAHRKILLCVVALSIIGTTHSLNKLNFNF"
    1009..1134
    /gene="Cj0344"
CDS
    1009..1134
    /gene="Cj0344"
    /note="Cj0344, unknown, len: 41 aa: no hp match"
    /codon_start=1
    /transl_table=11
    /product="hypothetical protein Cj0344"
    /protein_id="CAB74181.1"
    /db_xref="GI:6967819"
    /translation="MFQNIIRKYKDFILFILNLKONLYLLIKINLDFKNHKSINF"
    1299..2549
    /gene="trpB"
    1299..2549
    /gene="trpB"
    /EC_number="4.1.3.27"
    /note="Cj0345, trpB, possible anthranilate synthase
    component I, len: 416 aa: similar in C-terminal half to
    many e.g. TRPE_CLOTH anthranilate synthase component I (EC
    4.1.3.27) (494 aa), fasta scores: opt: 784 z-score: 1209.9
    E(): 0, 47.0% identity in 281 aa overlap, 35.6% identity
    in 365 aa overlap to HP1282. Contains pfam match to entry
    PF00425 chorismate_bind, chorismate binding enzyme, score
    309.50, E-value 3.9e-89"
    /codon_start=1
    /transl_table=11
    /product="putative anthranilate synthase component I"
    /protein_id="CAB74182.1"
    /db_xref="GI:6967820"
    /translation="MFVKNNVFYROIILKFNFSYAPDLTKVIIGIDCDYIDANELS
    YLEFKKYYEALSKKICDFAGFCFVSANFVSLPEKIPILSSKNNDI.LFLFANAKA
    KEVLISCDIFOVYVLSKQDICKOVANFDEYLSALNPSAYMFPPSKGVVIGSSPE
    FLKTRKRRLIYLAIPAGTRNLNENCDLALENDLSEKMLVDELANDSKPF
    ISELEDCDRGIYGVAGVLFNPNEDITAILIRCAFFPDQKAVYLASGAGIYQSSQK
    EYAEICARKKALLAVFENLKKRNF"
    1743..2522
    /gene="trpE"
    /note="Pfam match to entry PF00425 chorismate_bind,
    chorismate binding enzyme, score 309.50, E-value 3.9e-89"
    2546..3103
    /gene="trpD"
    /note="Pfam match to entry PF00117 GATase, Glutamine
    amidotransferases class-I, score 252.00, E-value 8.4e-72"
    2546..4147
    /gene="trpD"
    2546..4147
    /gene="trpD"
    /EC_number="4.1.3.27"
    /note="Cj0346, trpD (trpCD), probable anthranilate
    synthase component II, len: 533 aa: (contains glutamine
    amidotransferase and anthranilate
    phosphoribosyltransferase) similar to many e.g. TRPG_ECOLI
    anthranilate synthase component II (EC 4.1.3.27) (530 aa),
    fasta scores: opt: 866 z-score: 781.3 E(): 0, 32.6%
    identity in 528 aa overlap, N-terminus has 34.6% identity
    to HP1281, C-terminus is 33.2% identity to HP1280.
    Contains PS00442 Glutamine amidotransferases class-I
    active site and Pfam matches to entry PF00117 GATase,
    Glutamine amidotransferases class-I, score 252.00, E-value
    8.4e-72 and to entry PF00591 Glycosyltransferase, glycosyl
    transferase family, score 138.60, E-value 1.1e-37"
    /codon_start=1
    /transl_table=11
    /product="anthranilate synthase component II"
    /protein_id="CAB74183.1"
    /db_xref="GI:6967821"
    /translation="MILLINDYDFVNVKSMLEQISNDEILVRRDAISLSIKINLN
    PTHILISPGKPHSOSGICLIFKRALINIPVLCIGLGHQALALAFDLSLVKKQDEPMHA
    KNSLIQCKRENELSNLPSNFVSVARHSHLEKQISDELIELALDEKGVIMALGHKMLP
    YGVQHPESYFSEYGIQIFSNLFLKQDIKPKQENPLSFYLOKMSNHFLQSDPDEQ

```

```

misc_feature
    /gene="trpD"
    /note="PS00442 Glutamine amidotransferases class-I active
    site"
    3143..3589
    /gene="trpD"
    /note="Pfam match to entry PF00591 glycosyltransferase,
    glycosyl transferase family, score 138.60, E-value
    1.1e-37"
    4134..4733
    /gene="trpP"
    4134..4733
    /gene="trpP"
    /EC_number="5.3.1.24"
    /note="Cj0347, trpP, probable
    N-(5'-phosphoribosyl)anthranilate isomerase, len: 199 aa:
    similar to many trpP e.g. TRPF_IACCA
    N-(5'-phosphoribosyl)anthranilate isomerase (199 aa) (EC
    5.3.1.24) fasta scores: opt: 271 z-score: 352.4 E():
    2.3e-12, 31.0% identity in 200 aa overlap, and to the trpP
    domain of many trpC proteins e.g. TRPC_SALT1
    indole-3-glycerol phosphate synthase, fasta scores: opt:
    307 z-score: 394.5 E(): 1e-14, 30.8% identity in 201 aa
    overlap, 38.2% identity to C-terminus of HP1279 (trpC)
    N-(5'-phosphoribosyl)anthranilate (PRA) isomerase, score
    102.30, E-value 9.5e-27"
    /codon_start=1
    /transl_table=11
    /product="N-(5'-phosphoribosyl)anthranilate isomerase"
    /protein_id="CAB74184.1"
    /db_xref="GI:6967822"
    /translation="MLKLRKICGIDKKNKQDLAFNIDFGLIFAKSPRRVLEQARN
    LSAIFHEKDKRVGVFVDEMLQILKICKEAKLDGIQIRTKKEFEILKQNVFVW
    QVSVNSLDLKEISFANLVLFPDAKQILKFGNDSISDMLLSYTKDFLIAGIGLDN
    VHAVKTGARITLDLNSKLEDEKLDINKIKOILKELRK"
    4143..4721
    /gene="trpF"
    /note="Pfam match to entry PF00697 PRAI,
    N-(5'-phosphoribosyl)anthranilate (PRA) isomerase, score
    102.30, E-value 9.5e-27"
    4730..5908
    /gene="trpB"
    4730..5908
    /gene="trpB"
    /EC_number="4.2.1.20"
    /note="Cj0348, trpB, probable tryptophan synthase beta
    chain, len: 392 aa: highly similar to many e.g. TRPB_THEMA
    tryptophan synthase beta chain (EC 4.2.1.20) (389 aa),
    fasta scores: opt: 1476 z-score: 2082.2 E(): 0, 59.9%
    identity in 384 aa overlap, 56.4% identity to HP1278.
    Contains PS00168 Tryptophan synthase beta chain
    pyridoxal-phosphate attachment site, PS00017
    ATP/GTP-binding site motif A (P-loop), and Pfam match to
    entry PF00247 trp-syntB, tryptophan synthases, beta chain,
    score 806.40, E-value 1e-238"
    /codon_start=1
    /transl_table=11
    /product="tryptophan synthase beta chain"
    /protein_id="CAB74185.1"
    /db_xref="GI:6967823"
    /translation="MKKAYVGDGFGQPIPESSAMFALNELSQAFLKESKDKLFEKLENE
    LKTVYGRPTPLVFARANKSKAYQHEITYLRKEDLVNHTGAHKINNAIAQALLAKMGKKR
    ILAIFGAGOHGATATAALALDECEIYMGATVQROALNVYKMWELGAKIHAVQSL
    KVLCAITTAIAQAVGDIKNIFVYGVSAVGPYPYKVMHVFOSIIGKECKMOLOKLAK
    KVDYIIAAVGVGNAAGIFVDFIDENKMLIGIAGGIGIDTPYHAATLTKKGITGIH
    GMKTKVLQDDLGNIPLVHVSAGLDYPOIGPLHAFLESKRACQVHAISDECKQALTK

```

```

LCKEKGIIAIESSHALAFLEKLCPTLKKKSIVYVNLGRDCKDMQMRDVKKVIITG
Query Match      15.4%: Score 111.8: DB 1: Length 308601:
Best Local Similarity 74.4%: Pred. No. 1,9e-09:
Matches 154: Conservative 0: Mismatches 52: Indels 1: Gaps 1:

Qy 217 aagactcgtgtaaaaaaagaatgaactaagtggggcgtagctcagatggaagacctgac 276
      ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 81620 AAGATCATGATGTAAACCTAATGTTTATATGGCAATTAAGCTCAGCTGGGAGACGGCTCT 81679
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 277 ttccaagcagggggttcaggatgctcaactctctctctcctaccagaagaaggacctta 336
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 81680 TTGCACGACGAGAGGTACGCGGTTCCATCCCGCTATTCTCCACCA-TTTATTATGAAGGCCCTA 81738
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 337 tagctcagctcgtgttagagtcgcacgcctcgataagcagtcagtcagtcagtcagtcact 396
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 81739 TACCTCAGCTGCTGTAGAGAGCACCCCTGTATAGGCTGAGGTACCAAGTTCAAGTCTGTT 81798
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 397 agggccaccacatctgcacatgacaa 423
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 81799 AGGCCACCATTAATAAAGATTGAA 81825
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 14
CJ11168X1
LOCUS CJ11168X1 314150 bp DNA BCT 08-JUL-2000
DEFINITION Campylobacter jejuni NC011168 complete genome; segment 1/6.
ACCESSION AL139074 AL111168
VERSION AL139074.2 GI:6967505
KEYWORDS
SOURCE
ORGANISM Campylobacter jejuni.
          Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
          Campylobacter.
REFERENCE 1 (bases 1 to 314150)
          Parkhill,J., Wren,B.W., Mungall,K., Kelley,J.M., Churcher,C.,
          Basham,D., Chillingworth,T., Davies,R.M., Feltwell,T., Holtrold,S.,
          Jagels,K., Karlyshev,A., Moule,S., Pallen,M.J., Penn,C.W.,
          Quail,M., Rajandream,M.A., Rutherford,K.M., Vanyller,A.,
          Whitehead,S. and Barrall,B.G.
          The genome sequence of the food-borne pathogen Campylobacter jejuni
          reveals hypervariable sequences
          Nature 403 (6770), 665-668 (2000)
JOURNAL MEDLINE
REFERENCE 2 (bases 1 to 314150)
          Parkhill,J.
          Direct Submission
          Submitted (09-FEB-2000) Submitted on behalf of the Campylobacter
          sequencing team, Sanger Centre, Wellcome Trust Campus,
          Hinxton, Cambridge CB10 1SA E-mail: parkhill@sanger.ac.uk
COMMENT Notes:
          Details of C. jejuni sequencing at the Sanger Centre are available
          on the World Wide Web.
          (URL, http://www.sanger.ac.uk/Projects/C_jejuni/).
FEATURES
source
location/Qualifiers
1. 314150
   /organism="Campylobacter jejuni"
   /strain="NCTC 11168"
   /db_xref="taxon:197"
1. .1323
   /gene="dnaA"
1. .1323
   /gene="dnaA"
   /note="CJ0001, dnaA, probable chromosomal replication
   initiator protein, len: 440 aa; similar to many e.g.
   DNA-ECOLI (467 aa), Iasba scores; opt: 839 z-score: 949.6
   E): 0, 32.3% identity in 470 aa overlap, 39.9% identity
   to HP1529. Contains PS00017 Arp/GTP-binding site motif A
   (P-loop) and Pfam match to entry PF00308 bac_dnaA
   Bacterial dnaA protein, score 419.90, E-value 4e-141"
   /codon_start=1
   /transl_start=11
   /product="chromosomal replication initiator protein"

```

```

/protein_id="CA872494.1"
/db_xref="GI:6967506"
/translation="MNPSTQLNLEUKKELSENENYLSLNFKNESQKADLLVFNAP
ELMAKFETITGKGKIHAIFYEVSOGNNALINIIOAQSAOKSNKSTIDIAHAKASTIIL
PSFTFESTVEDNSKKVAYAGCKAIAHKMDIGLYLPDIYPVPTGLTHLAGGNNA
LEMFKATVIAENSENFIDENFSNLKSGSLDRPFEXRANCVDLLIIDVOFGTGRKIQGF
FEFLIKNEKINDDGOIIMTSNDPNPMMLKGTTEELSKRFRAHGIIADIPOPLDTYAI
IKCEEDNIINSNDINOINIASGDNRREIEGIISLANYATIIISOETTELDELASVK
HIKEKENITRIDOLLSJCNKERIKRPDYKSSKLTONIVYARRLVITYLAALTALMTM
OLAVFMKHTHTAISHWKKTITEMENDASLKAKIEELKNILKVSOS"
301..1239
/gene="dnaa"
/note="Pfam match to entry PF00308 bac.dnaa, Bacterial
dnaa protein, score 419.90, E-value 4e-141"
427..450
/gene="dnaa"
/note="PS00017 ATP/GTP-binding site motif A (P-loop)"
1483..2535
/gene="dnan"
/note="Pfam match to entry PF00712 DNA_pol3 beta, DNA
polymerase III beta subunit, score 119.80, E-value
5.2e-32"
1483..2550
/gene="dnan"
1483..2550
/gene="dnan"
/ec_number="2.7.7.7"
/note="Cj0002, dnaX, probable DNA polymerase III, beta
chain, len: 355 aa; similar to e.g. Dph_ECOLI DNA
polymerase III, beta chain (EC 2.7.7.7) (366 aa), fasta
scores: opt: 34.9 z-score: 372.3 E(): 1.7e-13, 19.6%
identity in 367 aa overlap, 34.2% identity to Hp0500.
Contains Pfam match to entry PF00024 DNA_topoisotII,
DNA topoisomerase II (N-terminal region), score 915.20,
E-value 1.9e-271, and to entry PF00986 DNA_gyraseB_C, DNA
gyrase B subunit, carboxyl terminus, score 154.00, E-value
2.6e-42"
/codon_start=1
/transl_table=11
/product="DNA gyrase subunit B"
/protein_id="CA872496.1"
/db_xref="GI:6967508"
/translation="MDENGASNIKVLKGLEAVRKRPQMYIGDTNIGLHHMIYEVD
NSIDEVASGHCDIIDEITGESCIYSODGRGI PDMHPTEMMTLTVLTVAIHACKG
EKDTQYVAGSGHDVGSVNALSKSIVATVRNGEIRROFSGSKVISPFYGICKS
KGTGIIEMPDMDIOFEVTEDDEILAKRRRELATINKRTINFRDNRYGKHSHFHREG
GISOFVDDIKKKALLNTAFSEVSDDEDVAVEALLINDTISENLSVNNIKTIIPDGCT
DEAPFRMGILRVATSIENASRSREDNKITIGDVDRGLLIAIVSVKPRPEOGEOTGK

```

misc_feature

/note="Pfam match to entry PF00204 DNA topoisom II (N-terminal region), score 915.20, E-value 1.9e-271"

3830. .3856

/gene="gyrB"

/note="PS00177 DNA topoisomerase II signature"

4649. .4852

/gene="gyrB"

/note="Pfam match to entry PF00986 DNA gyraseB_C, DNA gyrase B subunit, carboxyl terminus, score 154.00, E-value 2.6e-42"

complement(4916. .5257)

/gene="Cj0004c"

complement(4916. .5257)

/gene="Cj0004c"

/note="Cj0004c, possible periplasmic protein, len: 113 aa, No Hp match. Contains possible N-terminal signal sequence"

/codon_start=1

/transl_table=11

/product="putative periplasmic protein"

/protein_id="CAB72497.1"

/db_xref="GI:6967509"

/translation="MKKIIILALFLASMAQNLINPDGLIIDPSPIVANCILAC HSNLLTNHNASRKMALAIIRMQDSELMIEPEDEKILANTLENYGEEKIDTRRI PLAILLONRTH"

complement(5260. .6498)

/gene="Cj0005c"

complement(5260. .6498)

/gene="Cj0005c"

/note="Cj0005c, possible molybdenum containing oxidoreductase, len: 412 aa; similar to many eukaryotic oxidoreductases e.g. SUOX, HUMAN sulfite oxidase precursor (488 aa), fasta scores: opt: 543 z-score: 338.2 E(): 1.4e-11, 29.8% identity in 372 aa overlap and NIA-PTNH nitrate reductase from Petunia hybrida (909 aa), fasta scores: opt: 281 z-score: 312.5 E(): 3.8e-10, 28.9% identity in 395 aa overlap. No Hp match. Contains Pfam match to entry PF00174 oxidored_molYb, Oxidoreductase molybdopterin binding domain, score 45.20, E-value 1e-12"

/codon_start=1

/transl_table=11

/product="putative molybdenum containing oxidoreductase"

/protein_id="CAB72498.1"

/db_xref="GI:6967510"

/translation="MKQNDQEKNRKDFLNKINIGLFGISVLNFSFENPLGSKALAKE LPDRLEICKKPLIYHGKRPPLAETELIYALDSPTKPFNFVANNGLPSTLPIKRLR KGWLEIDGESIIINKKSYTIEDLKKEKRYTVALITECGNRSRYVISTGTOMGTG AVACGRMVGKIDKLDKDCGIRKNDAYIGYVGTDLKNEETSPISKGVPSKALQDE TLIIMAVEGKQPLVNYGKPLRYVCGGTPASTSKWLYKTIVNKKIHDKEGMSKKYV VSNPKRGDFNTKGMKLTIESMPLRSVITNKNSEIKRARKKEVAGKMAAELEVESEV YVSDNYGQYTWKRAVEKPLNRLAMQWMSAQISIPTKGYEITWARIADISGQSNPVLA QMNPGCYINNAACHVNVYGV"

complement(5950. .6138)

/gene="Cj0005c"

/note="Pfam match to entry PF00174 oxidored_molYb, Oxidoreductase molybdopterin binding domain, score 45.20, E-value 1e-12"

6703. .8010

/gene="Cj0006"

6703. .8010

/gene="Cj0006"

/note="Cj0006, probable integral membrane protein, len: 435 aa; similar to e.g. Y325_HAfin hypothetical protein

Query Match	15.4%	Score 11.8	DB 1	Length 314150
Best Local Similarity	74.4%	Pred. No. 1.9e-09		
Matches 154	Conservative 0	Mismatches 52	Indels 1	Gaps 1

QY	217	aagacttggtaaaaaaagaatgaactaatatgagggcgtagctcagatgagagacactgcc	276
Db	40838	AAGATTGATCATATAACCTAATGTTATATGGGAATAATAGCTACGCTGCGGAGACGGCTGCT	40897
QY	277	tttcaagacagggggttaaggaagttaactctctctgctctccaccagaagaaggccta	336
Db	40898	TTTCACAGCAGAGAGTACGGCGTTCCATCCCGCTAATTCACCA-TTATATTAAGGCGCTTA	40956
QY	337	ttagctacgttggttagagcgacgcagctgataaagcgtlgaagtagtgaagtcacgttact	396
Db	40957	TAGCTACGTGTTAGAGTGCACCCCTGATAGAGGTGAGGTACAAAGTTCAAGTCTGTT	41016
QY	397	aggccaccacatatgacatgacataa 423	
Db	41017	AGGCCACCATTAATAAAGATTGAAATA 41043	

LOCUS	CJ11168X3	317511 bp	DNA	BCF	08-JUL-2000
DEFINITION	Campylobacter jejuni NCTC11168 complete genome; segment 3/6.				
ACCESSION	AL139076				
VERSION	AL139076.2				
KEYWORDS	GI:5968128				
SOURCE	-				
ORGANISM	Campylobacter jejuni. Campylobacter jejuni. Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group; Campylobacter.				
REFERENCE	1 (bases 1 to 317511) Parkhill, J., Wren, B.W., Mungall, K., Kelsey, J.M., Churcher, C., Basham, D., Chillingworth, T., Davies, R.M., Feltham, T., Holt, R.D., Jolley, K.A., Karpman, A., Moule, S., Pallen, M.J., Penn, C.W., Quail, M., Rajandream, M.A., Rutherford, K.M., Van Vliet, A., Whitehead, S. and Barrett, B.G. The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hypervariable sequences				
AUTHORS	Nature 403 (6770), 665-668 (2000)				
JOURNAL	2 (bases 1 to 317511) Parkhill, J.				
MEDLINE	Direct Submission				
REFERENCE	Submitted (09-FEB-2000) Submitted on behalf of the Campylobacter sequencing team, Sanger Centre, Wellcome Trust Sanger Campus, Hinxton, Cambridgeshire CB10 1SA E-mail: parkhill@sanger.ac.uk				
TITLE	Details of C. jejuni sequencing at the Sanger Centre are available on the World Wide Web.				
COMMENT	(URL, http://www.sanger.ac.uk/Projects/C._jejuni/). Location/Qualifiers 1. 317511 /organism="Campylobacter jejuni" /strain="NCTC 11168" /db_xref="taxon:197" 119. 364 /gene="Cj0667" 119. 364 /gene="Cj0667" /note="Cj0667, unknown, len: 81 aa, similar to many hypothetical proteins e.g. YABO_BACT5 (86 aa), fasta scores: opt: 149 z-score: 259.2 E(1): 3.8e-07, 35.48 identity in 79 aa overlap. 43.6% identity to HP1423" /codon_start=1				

	/transl_table=11 /product-"hypothetical protein Cj0667" /protein_id="CAB72944.1" /db_xref="GI:6968129" /translation="MRVDFLNVNITRRRAISEDMCKSGVGICINGIVKASKEYVD DITTHFEFTGYTKYKVLPSPKSIPKNAQNYVKLV" 361..768
gene	/gene="Cj0668" /note="Cj0668, probable ATP/GTP-binding protein, len: 135 aa; similar to hypothetical proteins e-9, yJEE_ECOLI (153 aa), fasta scores: opt: 164 z-score: 205.3 E(): 0.00039, 33.8% identity in 80 aa overlap, 44.2% identity to Hp0716. Contains PS00017 ATP/GTP-binding site motif A (P-loop)." /codon_start=1 /transl_table=11 /product-"putative ATP /GTP-binding protein" /protein_id="CAB72945.1" /db_xref="GI:6968130"
CDS	/translation="MKELIAKNKIETLMLOIMPEKEVVLLGGDLASKTSILVAWKF LGIDRVSDPSFPMOKENEDICTHYDIQESELGLNGLFENPFEGKLHWENG GENLKTLRKIGSTIQIKTISKDKRKYEYE" 442..465
misc_feature	/gene="Cj0668" /note="PS00017 ATP/GTP-binding site motif A (P-loop)" 761..1489
gene	/gene="Cj0669" 761..1489
CDS	/gene="Cj0669" /note="Cj0669, probable ABC-transporter ATP-binding protein, len: 242 aa; highly similar to many e-9. yHBC_ECOLI, probable ABC transporter ATP-binding protein (240 aa), fasta scores: opt: 840 z-score: 1144.2 E(): 0, HP0715. Contains PS00017 ATP /GTP-binding site motif A (P-loop) and Pfam match to entry PF00005 ABC_tran, ABC transporters." /codon_start=1 /transl_table=11 /product="ABC-transporter ATP-binding protein" /protein_id="CAB72946.1" /db_xref="GI:6968131"
	/translation="MSKETVLNEKITKTIIHGISLEVNSEGVVGLPGAGAKTT TRYMTGLISPSSGNVLGDLDVTDPNLKRARRSIGYPRESSIFRULSVEDNLLA AQYFYDKNITLHRKVQMELLSIEPIRLKGISGGERCEIARSLMCPKKLLL DEFPACVDIVAIEIoTLIKELRKRGIGVLTDHNVERFLALCDRAYIRSSSLLASG MADELTNRKDVKYYLAGAEFKILD" 845..1396
misc_feature	/gene="Cj0669" /note="Pfam match to entry PF00005 ABC_tran, ABC transporters, score 221.60, E-value 1.e-62" 866..889
misc_feature	/gene="Cj0669" /note="PS00017 ATP/GTP-binding site motif A (P-loop)" 1486..2718
	/note="Pfam match to entry PF00309 Sigma54_fact rs, Sigma-54 factors family, score 42.30, E-value 8.4e-20" 1489..2739
gene	/gene="rpon" 1489..2739
CDS	/gene="rpon" /note="Cj0670, rpon, probable RNA polymerase sigma-54 factor, len 416 aa; similar to many e-9. RP54_BACSU RNA polymerase sigma-54 factor (436 aa), fasta scores: opt: 557 z-score: 603.0 E(): 2.7e-26, 28.9% identity in 443 aa overlap, and RP54_ECOLI (477 aa), fasta scores: opt: 365 z-score: 483.2 E(): 1.3e-19, 28.8% identity in 459 aa overlap, 47.4% identity to Hp0714. Contains PS00718 Sigma-54 factors family signature 2, Pfam match to entry PF00309 sigma54_factors, and helix-turn-helix motif at aa 303-324 (Score 1227; +3.37 SD)." /codon_start=1
	/transl_table=11 /product-"RNA polymerase sigma-54 factor" /protein_id="CAB72947.1" /db_xref="GI:6968132" /translation="MLKOKITPOAPKRTISOQLRSWLPIIOANTENKLNDRFAEPN FLNVQSIOTHDGKNYNFDSEFFAHNNASDGKLAKSYVELLEOQLPLPLEPS SOLEAKKIIICEINECGFHEDEFERLEYESTLEEIERVARPKFLDPYGAKDYKEAF PALEMFMLEDIDEFCMLIMDVENIONTYREPLYEAVALVRKSFPPLEFEDS IIVDFIVKENEDIKVKINDDYPELSIoTDLENDFLSHYIREKANLVDAIAMRK TLRYIGIMEIYGYDFEMKEIKPMPFKDALDENASTISAANVKYLSCERGILI LRREFAPALDEGETSNVGEKFEVAMVMKEDBNRP LSKILELIKEFKYVIDGR ITRYRKHLNIASSSTRKITYELGS" 2656..2679
misc_feature	/gene="rpon" /note="PS00718 Sigma-54 factors family signature 2" 2903..4327
gene	/gene="dcub" 2903..4327
CDS	/gene="dcub" /note="Cj0671, dcub, probable anaerobic C4-dicarboxylate transporter, len: 474 aa; highly similar to e.g. DCUB_ECOLI anaerobic C4-dicarboxylate transporter (446 aa);opt: 1280 z-score: 2918.6 E(): 0, 69.1% identity in 466 aa overlap. No hp ortholog. Also similar to Cj0088, dcua (37.0% identity in 465 aa overlap)" /codon_start=1 /transl_table=11 /product-"putative anaerobic C4-dicarboxylate transporter" /protein_id="CAB72948.1" /db_xref="GI:6968133"
	/translation="MDFLTSLSEAGOFATOIITVICLFGARKGIALGLIGIII MLVFENHPGPADIVMLTIAAVVASATVOASGLDVMOIERILRNRPKELITITI APFVCILITLCGTGHVYTIMPITIIDAIKNGIRREPBMXAASISSOMGIASPVSA AVSLTFALLLNANHKLAGEPDGYINTLOTISTLEGRCVCTIFPSFRKDDLDKDEVC EKDKPERFKYYGDSKTLVGLPRKSMVAMVIFLGAIALVALLGVPFLRPMWGCV VKNQGPSVDALGNPMADVNSVSVIOLMDLAGSLITIFTTIDAKKIGSNEIFSMMI ALVAVEGISMAADTWFAVHTPPMKRALDIVKEHMYAYAMILLISFVNSQAASI EVPLALGIVEPGEVIFAFAACYGYIILPTVPSLATIQFORSCTHIKRFVINHSFI LGLIGVITSCAGYFIAMAAGYL" 4469..4657
gene	/gene="Cj0672" 4469..4657
CDS	/gene="Cj0672" /note="Cj0672, possible periplasmic protein, len: 62 aa; no hp match. Contains possible N-terminal signal sequence and second hydrophobic domain" /codon_start=1 /transl_table=11 /product-"putative periplasmic protein" /protein_id="CAB72949.1" /db_xref="GI:6968134"
	/translation="MRKGYPDIIFFALLLLAFGLCFICFCEIQTKDTRMIFLLVL SLILALYLEVALTYPERK" 4667..6410
gene	/gene="kdpA" 4667..6410
CDS	/gene="kdpA" /gc_number="3,6,1.36" /note="Cj0676, kdpA, probable potassium-transporing ATPase A chain pseudogene, len: 1744 bp; highly similar to e-9. ARKA_ECOLI potassium-transporing ATPase A chain (GC 3.6-1.36) (557 aa). No hp match. Note thay kdpB (Cj0677) is intact, while kdpC (Cj0678) is a pseudogene" /codon_start=1 /pseudo /transl_table=11 /product-"pseudogene (potassium-transporing ATPase A chain)" 5521..5529
repeat_region	/note="G(9)" 6371..8416
gene	/gene="kdpB"

